

1/25

FIG. 1A.

Sequence length 2175

CACGCGTCCGCAAATTTCTGATTCTTTGAATTAGGATTCCAGATGGGGGCTCATTCTACAGCCCCAACATTCTCT
ATAGCCGTTATCACTGCCATCACCCTGCCACCAGCATCTTCTTGAGATTCCACCCCTGCTCCCCAGAGACTTCCTGC
TTTGAAAGTGAGCAGAAAGGAAGCTCTCAGAAAAATCTCTAGTGGTGGCTGCCGTCGCTCCAGACAATCGGAATCCTGC

M	G	W	L	F	L	K	V	L	L	A	G	V	S	F	S	G	17			
CTTCACCACC	ATG	GGC	TGG	CTT	TTT	CTA	AAG	GTT	TTG	TTG	GCG	GGA	GTG	AGT	TTC	TCA	GGA	51		
F	L	Y	P	L	V	D	F	C	I	S	G	K	T	R	G	Q	K	P	N	37
TTT	CTT	TAT	CCT	CTT	GTG	GAT	TTT	TGC	ATC	AGT	GGG	AAA	ACA	AGA	GGA	CAG	AAG	CCA	AAC	111
F	V	I	I	L	A	D	D	M	G	W	G	D	L	G	A	N	W	A	E	57
TTT	GTG	ATT	ATT	TTG	GCC	GAT	GAC	ATG	GGG	TGG	GGT	GAC	CTG	GGA	GCA	AAC	TGG	GCA	GAA	171
T	K	D	T	A	N	L	D	K	M	A	S	E	G	M	R	F	V	D	F	77
ACA	AAG	GAC	ACT	GCC	AAC	CTT	GAT	AAG	ATG	GCT	TGC	GAG	GGA	ATG	AGG	TTT	GTG	GAT	TTC	231
H	A	A	A	S	T	C	S	P	S	R	A	S	L	L	T	G	R	L	G	97
CAT	GCA	GCT	GCC	TCC	ACC	TGC	TCA	CCC	TCC	CGG	GCT	TCC	TTG	CTC	ACC	GGC	CGG	CTT	GGC	291
L	R	N	G	V	T	R	N	F	A	V	T	S	V	G	G	L	P	L	N	117
CTT	CGC	AAT	GGA	GTC	ACA	CGC	AAC	TTT	GCA	GTC	ACT	TCT	GTG	GGA	GGC	CTT	CCG	CTC	AAC	351
E	T	T	L	A	E	V	L	Q	Q	A	G	Y	V	T	G	I	I	G	K	137
GAG	ACC	ACC	TTG	GCA	GAG	GTG	CTG	CAG	CAG	GCG	GGT	TAC	GTG	ACT	GGG	ATA	ATA	GGC	AAA	411
W	H	L	G	H	H	G	S	Y	H	P	N	F	R	G	F	D	Y	Y	F	157
TGG	CAT	CTT	GGA	CAC	CAC	GGC	TCT	TAT	CAC	CCC	AAC	TTC	CGT	GGT	TTT	GAT	TAC	TAC	TTT	471
G	I	P	Y	S	H	D	M	G	C	T	D	T	P	G	Y	N	H	P	P	177
GGA	ATC	CCA	TAT	AGC	CAT	GAT	ATG	GGC	TGT	ACT	GAT	ACT	CCA	GGC	TAC	AAC	CAC	CCT	CCT	531
C	P	A	C	P	Q	G	D	G	P	S	R	N	L	Q	R	D	C	Y	T	197
TGT	CCA	GCG	TGT	CCA	CAG	GGT	GAT	GGA	CCA	TCA	AGG	AAC	CTT	CAA	AGA	GAC	TGT	TAC	ACT	591
D	V	A	L	P	L	Y	E	N	L	N	I	V	E	Q	P	V	N	L	S	217
GAC	GTG	GCC	CTC	CCT	CTT	TAT	GAA	AAC	CTC	AAC	ATT	GTG	GAG	CAG	CCG	GTG	AAC	TTG	AGC	651
S	L	A	Q	K	Y	A	E	K	A	T	Q	F	I	Q	R	A	S	T	S	237
AGC	CTT	GCC	CAG	AAG	TAT	GCT	GAG	AAA	GCA	ACC	CAG	TTC	ATC	CAG	CGT	GCA	AGC	ACC	AGC	711
G	R	P	F	L	L	Y	V	A	L	A	H	M	H	V	P	L	P	V	T	257
GGG	AGG	CCC	TTC	CTG	CTC	TAT	GTG	GCT	CTG	GCC	CAC	ATG	CAC	GTG	CCC	TTA	CCC	GTG	ACT	771
Q	L	P	A	A	P	R	G	R	S	L	Y	G	A	G	L	W	E	M	D	277
CAG	CTA	CCA	GCA	GCG	CCA	CGG	GGC	AGA	AGC	CTG	TAT	GGT	GCA	GGG	CTC	TGG	GAG	ATG	GAC	831
S	L	V	G	Q	I	K	D	K	V	D	H	T	V	K	E	N	T	F	L	297
AGT	CTG	GTG	GGC	CAG	ATC	AAG	GAC	AAA	GTT	GAC	CAC	ACA	GTG	AAG	GAA	AAC	ACA	TTC	CTC	891
W	F	T	G	D	N	G	P	W	A	Q	K	C	E	L	A	G	S	V	G	317
TGG	TTT	ACA	GGA	GAC	AAT	GGC	CCG	TGG	GCT	CAG	AAG	TGT	GAG	CTA	GCG	GGC	AGT	GTG	GGT	951
P	F	T	G	F	W	Q	T	R	Q	G	G	S	P	A	K	Q	T	T	W	337
CCC	TTC	ACT	GGA	TTT	TGG	CAA	ACT	CGT	CAA	GGG	GGA	AGT	CCA	GCC	AAG	CAG	ACG	ACC	TGG	1011
E	G	G	H	R	V	P	A	L	A	Y	W	P	G	R	V	P	V	N	V	357

2/25

GAA GGA GGC CAC CGG GTC CCA GCA CTC CCA GCA CTG GCT TAC TGG CCT GGC AGA GTT CCA GTT AAT GTC	1071
T S T A L L S V L D I F P T V V A L A Q	377
ACC AGC ACT GCC TTG TTA AGC GTG CTG GAC ATT TTT CCA ACT GTG GTA GCC CTG GCC CAG	1131
A S L P Q G R R F D G V D V S E V L F G	397
GCC AGC TTA CCT CAA GGA CGG CGC TTT GAT GGT GTG GAC GTC TCC GAG GTG CTC TTT GGC	1191
R S Q P G H R V L F H P N S G A A G E F	417
CGG TCA CAG CCT GGG CAC AGG GTG CTG TTC CAC CCC AAC AGC GGG GCA GCT GGA GAG TTT	1251
G A L Q T V R L E R Y K A F Y I T G G A	437
GGA GCC CTG CAG ACT GTC CGC CTG GAG CGT TAC AAG GCC TTC TAC ATT ACC GGT GGA GCC	1311
R A C D G S T G P E L Q H K F P L I F N	457
AGG GCT TGT GAT GGG AGC ACG GGG CCT GAG CTG CAG CAT AAG TTT CCT CTG ATT TTC AAC	1371
L E D D T A E A V P L E R G G A E Y Q A	477
CTG GAA GAC GAT ACC GCA GAA GCT GTG CCC CTA GAA AGA GGT GGT GCG GAG TAC CAG GCT	1431
V L P E V R K V L A D V L Q D I A N D N	497
GTG CTG CCC GAG GTC AGA AAG GTT CTT GCA GAC GTC CTC CAA GAC ATT GCC AAC GAC AAC	1491
I S S A D Y T Q D P S V T P C C N P Y Q	517
ATC TCC AGC GCA GAT TAC ACT CAG GAC CCT TCA GTA ACT CCC TGC TGT AAT CCC TAC CAA	1551
I A C R C Q A A *	526
ATT GCC TGC CGC TGT CAA GCC GCA TAA	1578

CAGACCAATTTTATTCCACGAGGAGGAGTACCTGGAAATTAGGCAAGTTTGCTTCCAAATTTTCATTTTACCCTCTTT
ACAAACACACGCTTTAGTTTAGTCTTGGAGTTTAGTTTGGAGTTAGCCTTG CATATCCCTTCTGTATCCTGTCCCTCC
TCCACGCCGACCCGAGAGCAGCTGAGCTGCGCTGGCTCTGGGCACCCAGTGTGCCTTAATGGGAAGCACACGGGCTTGG
GAGTCAGGCACAGGTGCCAGCTCCAGCTTTTGA ACTTGGGCAATTGTTTAACCTAACCTGCAAGTTGATTTTGAGGGTT
AAATAAAGGCATACATGAAAAAAAAAAAAAAAAAAAA

FIG. 1B.

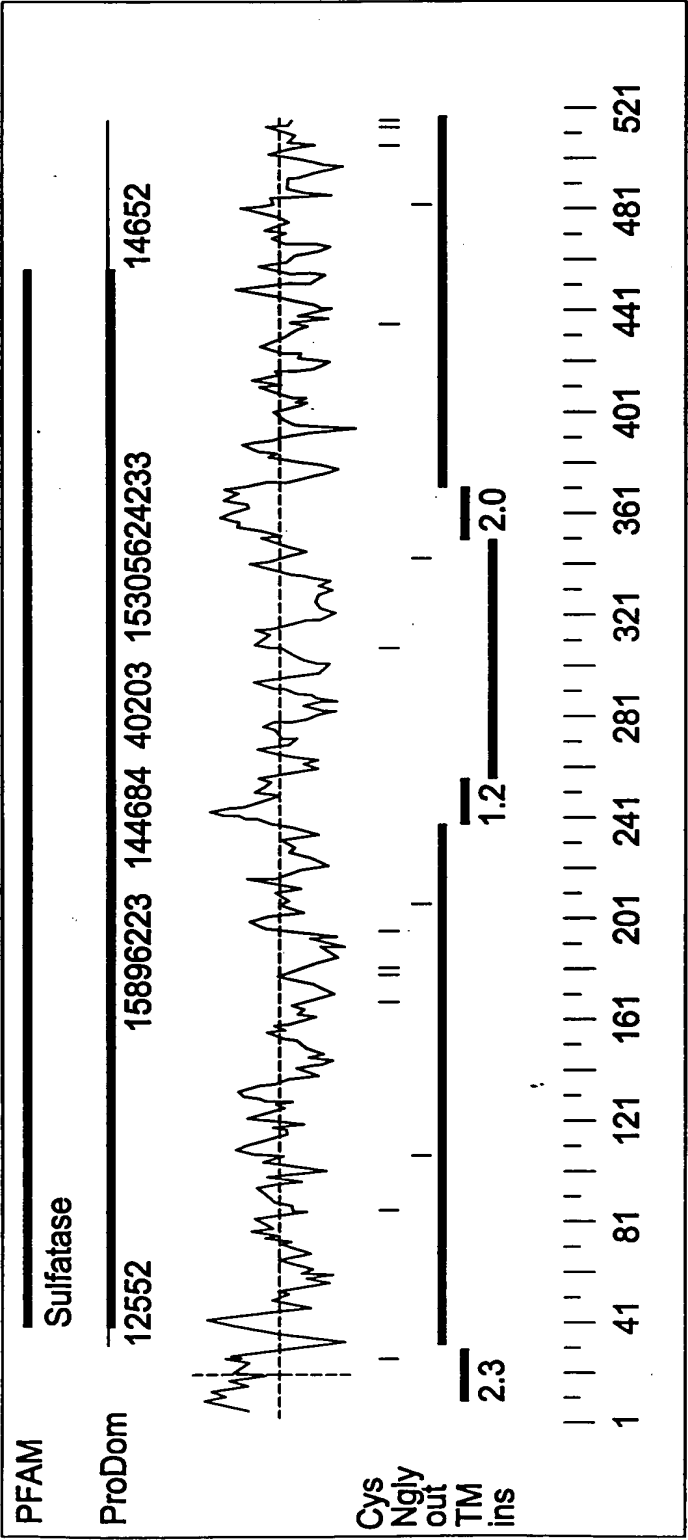


FIG. 2.

4/25

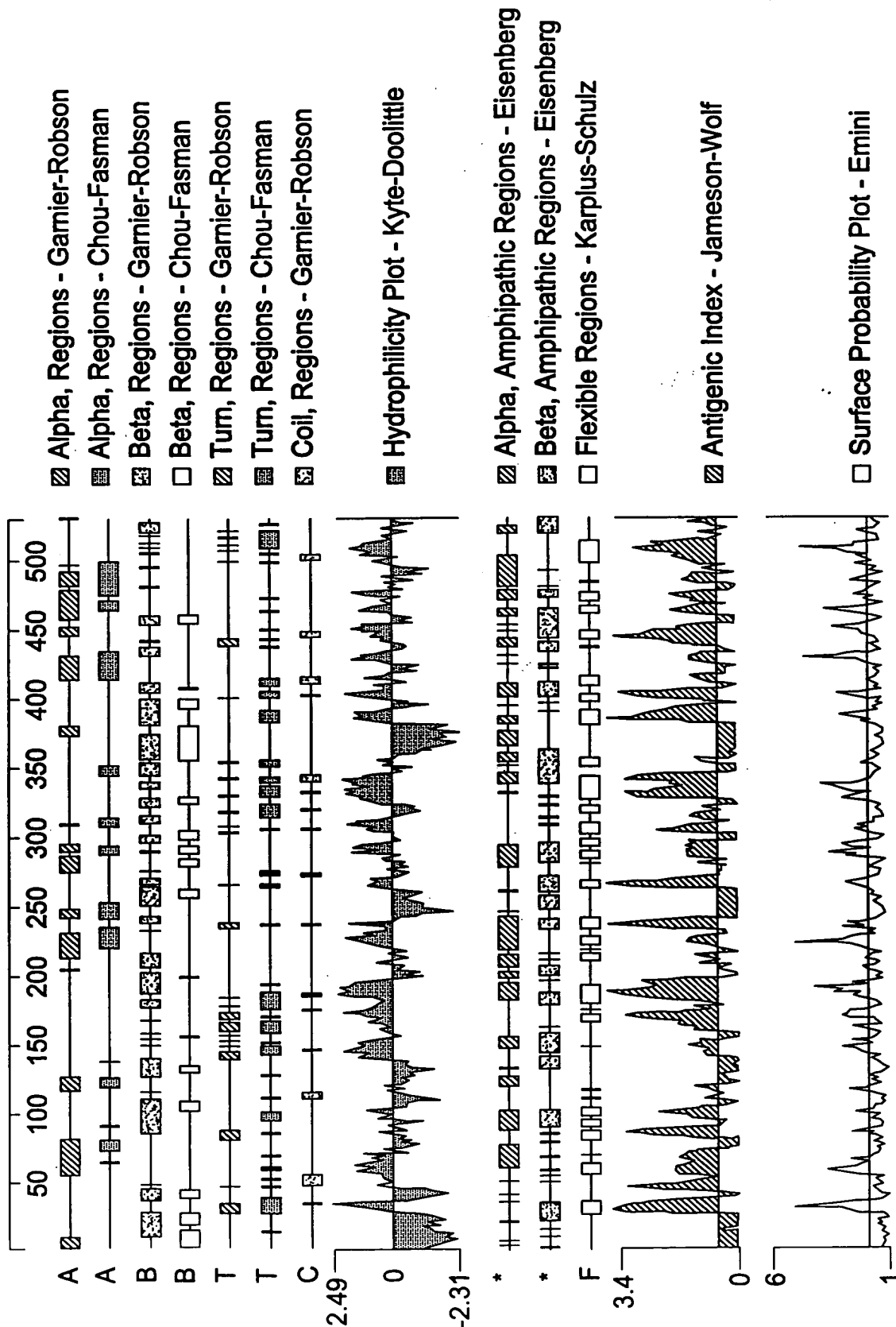


FIG. 3.

5/25

FIG. 4.

Prosite Pattern Matches

Prosite version: Release 12.2 of February 1995

>PS00001/PDOC00001/ASN_GLYCOSYLATION N-glycosylation site.

Query: 117 NETT 120

Query: 215 NLSS 218

Query: 356 NVTs 359

Query: 497 NISS 500

>PS00005/PDOC00005/PKC_PHOSPHO_SITE Protein kinase C phosphorylation site.

Query: 28 SGK 30

Query: 93 TGR 95

Query: 237 SGR 239

Query: 290 TVK 292

Query: 422 TVR 424

>PS00006/PDOC00006/CK2_PHOSPHO_SITE Casein kinase II phosphorylation site.

Query: 120 TLAE 123

Query: 290 TVKE 293

Query: 335 TTWE 338

Query: 364 SVLD 367

Query: 444 TGPE 447

Query: 499 SSAD 502

>PS00008/PDOC00008/MYRISTYL N-myristoylation site.

Query: 12 GVSFSG 17

Query: 33 GQKPNF 38

Query: 52 GANWAE 57

Query: 97 GLRNGV 102

Query: 113 GLPLNE 118

Query: 158 GIPYSH 163

Query: 328 GGSPAK 333

Query: 388 GVDVSE 393

Query: 418 GALQTV 423

Query: 435 GGARAC 440

>PS00009/PDOC00009/AMIDATION Amidation site.

Query: 382 QGRR 385

>PS00149/PDOC00117/SULFATASE_2 Sulfatases signature 2.

Query: 129 GYVTGIIGKW 138

6/25

FIG. 5A.

Input file Fbh23553fl.seq; Output File 23553.trans
Sequence length 4321

```
CCCACGCGTCCGGCTAATGAATCTTGGGGCCGGTGTCTGGGCCGGGGCGGCTTGATCGGCAACTAGGAAACCCAGGCGC
AGAGGGCCAGGAGCGAGGGCAGCGAGGATCAGAGGCCAGGCCCTTCCCGGCTGCCGGCGCTCCTCGGAGGTCAGGGCAGAT
GAGGAACATGACTCTCCCCCTTCGGAGGAGGAAGGAAGTCCCGCTGCCACCTTATCTCTGCTCCTCTGCCTCCTCCCTG
TTCCAGAGCTTTTTCTCTAGAGAAGATTTTGAAGGCGGCTTTTGTGCTGACGGCCACCCACCATCATCTAAAGAAGAT
AAACTTGGCAAATGACATGCAGGTTCTTCAAGGCAGAATAATTGCAGAAAATCTTCAAAGGACCCTATCTGCAGATGTT
CTGAATACCTCTGAGAATAGAGATTGATTATTCAACCAGGATACCTAATTCAAGAACTCCAGAAATCAGGAGACGGAGA

      M K Y S C C A L V L A 11
CATTGTGTCAGTTTTGCAACATTGGACCAAATACA ATG AAG TAT TCT TGC TGT GCT CTG GTT TTG GCT 33
V L G T E L L G S L C S T V R S P R F R 31
GTC CTG GGC ACA GAA TTG CTG GGA AGC CTC TGT TCG ACT GTC AGA TCC CCG AGG TTC AGA 93
G R I Q Q E R K N I R P N I I L V L T D 51
GGA CGG ATA CAG CAG GAA CGA AAA AAC ATC CGA CCC AAC ATT ATT CTT GTG CTT ACC GAT 153
D Q D V E L G S L Q V M N K T R K I M E 71
GAT CAA GAT GTG GAG CTG GGG TCC CTG CAA GTC ATG AAC AAA ACG AGA AAG ATT ATG GAA 213
H G G A T F I N A F V T T P M C C P S R 91
CAT GGG GGG GCC ACC TTC ATC AAT GCC TTT GTG ACT ACA CCC ATG TGC TGC CCG TCA CGG 273
S S M L T G K Y V H N H N V Y T N N E N 111
TCC TCC ATG CTC ACC GGG AAG TAT GTG CAC AAT CAC AAT GTC TAC ACC AAC AAC GAG AAC 333
C S S P S W Q A M H E P R T F A V Y L N 131
TGC TCT TCC CCC TCG TGG CAG GCC ATG CAT GAG CCT CGG ACT TTT GCT GTA TAT CTT AAC 393
N T G Y R T A F F G K Y L N E Y N G S Y 151
AAC ACT GGC TAC AGA ACA GCC TTT TTT GGA AAA TAC CTC AAT GAA TAT AAT GGC AGC TAC 453
I P P G W R E W L G L I K N S R F Y N Y 171
ATC CCC CCT GGG TGG CGA GAA TGG CTT GGA TTA ATC AAG AAT TCT CGC TTC TAT AAT TAC 513
I V C R N G I K E K H G F D Y A K D Y F 191
ACT GTT TGT CGC AAT GGC ATC AAA GAA AAG CAT GGA TTT GAT TAT GCA AAG GAC TAC TTC 573
T D L I T N E S I N Y F K M S K R M Y P 211
ACA GAC TTA ATC ACT AAC GAG AGC ATT AAT TAC TTC AAA ATG TCT AAG AGA ATG TAT CCC 633
H R P V M M V I S H A A P H G P E D S A 231
CAT AGG CCC GTT ATG ATG GTG ATC AGC CAC GCT GCG CCC CAC GGC CCC GAG GAC TAC GCC 693
P Q F S K L Y P N A S Q H I T P S Y N Y 251
CCA CAG TTT TCT AAA CTG TAC CCC AAT GCT TCC CAA CAC ATA ACT CCT AGT TAT AAC TAT 753
A P N M D K H W I M Q Y T G P M L P I H 271
GCA CCA AAT ATG GAT AAA CAC TGG ATT ATG CAG TAC ACA GGA CCA ATG CTG CCC ATC CAC 813
M E F T N I L Q R K R L Q T L M S V D D 291
ATG GAA TTT ACA AAC ATT CTA CAG CGC AAA AGG CTC CAG ACT TTG ATG TCA GTG GAT GAT 873
S V E R L Y N M L V E T G E L E N T Y I 311
```

7/25

FIG. 5B.

```
TCT GTG GAG AGG CTG TAT AAC ATG CTC GTG GAG ACG GGG GAG CTG GAG AAT ACT TAC ATC 933
I Y T A D H G Y H I G Q F G L V K G K S 331
ATT TAC ACC GCC GAC CAT GGT TAC CAT ATT GGG CAG TTT GCA CTG GTC AAG GGG AAA TCC 993
M P Y D F D I R V P F F I R G P S V E P 351
ATG CCA TAT GAC TTT GAT ATT CGT GTG CCT TTT TTT ATT CGT GGT CCA AGT GTA GAA CCA 1053
G S I V P Q I V L N I D L A P T I L D I 371
GGA TCA ATA GTC CCA CAG ATC GTT CTC AAC ATT GAC TTG GCC CCC ACG ATC CTG GAT ATT 1113
A G L D T P P D V D G K S V L K L L D P 391
GCT GGG CTC GAC ACA CCT CCT GAT GTG GAC GGC AAG TCT GTC CTC AAA CTT CTG GAC CCA 1173
E K P G N R F R T N K K A K I W R D T F 411
GAA AAG CCA GGT AAC AGG TTT CGA ACA AAC AAG AAG GCC AAA ATT TGG CGT GAT ACA TTC 1233
L V E R G K F L R K K E E S S K N I Q Q 431
CTA GTG GAA AGA GGC AAA TTT CTA CGT AAG AAG GAA GAA TCC AGC AAG AAT ATC CAA CAG 1293
S N H L P K Y E R V K E L C Q Q A R Y Q 451
TCA AAT CAC TTG CCC AAA TAT GAA CGG GTC AAA GAA CTA TGC CAG CAG GCC AGG TAC CAG 1353
T A C E Q P G Q K W Q C I E D T S G K L 471
ACA GCC TGT GAA CAA CCG GGG CAG AAG TGG CAA TGC ATT GAG GAT ACA TCT GGC AAG CTT 1413
R I H K C K G P S D L L T V R Q S T R N 491
CGA ATT CAC AAG TGT AAA GGA CCC AGT GAC CTG CTC ACA GTC CGG CAG AGC ACG CGG AAC 1473
L Y A R G F H D K D K E C S C R E S G Y 511
CTC TAC GCT CGC GGC TTC CAT GAC AAA GAC AAA GAG TGC AGT TGT AGG GAG TCT GGT TAC 1533
R A S R S Q R K S Q R Q F L R N Q G T P 531
CGT GCC AGC AGA AGC CAA AGA AAG AGT CAA CGG CAA TTC TTG AGA AAC CAG GGG ACT CCA 1593
K Y K P R F V H T R Q T R S L S V E F E 551
AAG TAC AAG CCC AGA TTT GTC CAT ACT CGG CAG ACA CGT TCC TTG TCC GTC GAA TTT GAA 1653
G E I Y D I N L E E E E E L Q V L Q P R 571
GGT GAA ATA TAT GAC ATA AAT CTG GAA GAA GAA GAA GAA TTG CAA GTG TTG CAA CCA AGA 1713
N I A K R H D E G H K G P R D L Q A S S 591
AAC ATT GCT AAG CGT CAT GAT GAA GGC CAC AAG GGG CCA AGA GAT CTC CAG GCT TCC AGT 1773
G G N R G R M L A D S S N A V G P P T T 611
GGT GGC AAC AGG GGC AGG ATG CTG GCA GAT AGC AGC AAC GCC GTG GGC CCA CCT ACC ACT 1833
V R V T H K C F I L P N D S I H C E R E 631
GTC CGA GTG ACA CAC AAG TGT TTT ATT CTT CCC AAT GAC TCT ATC CAT TGT GAG AGA GAA 1893
L Y Q S A R A W K D H K A Y I D K E I E 651
CTG TAC CAA TCG GCC AGA GCG TGG AAG GAC CAT AAG GCA TAC ATT GAC AAA GAG ATT GAA 1953
A L Q D K I K N L R E V R G H L K R R K 671
GCT CTG CAA GAT AAA ATT AAG AAT TTA AGA GAA GTG AGA GGA CAT CTG AAG AGA AGG AAG 2013
P E E C S C S K Q S Y Y N K E K G V K K 291
CCT GAG GAA TGT AGC TGC AGT AAA CAA AGC TAT TAC AAT AAA GAG AAA GGT GTA AAA AAG 2073
Q E K L K S H L H P F K E A A Q E V D S 711
CAA GAG AAA TTA AAG AGC CAT CTT CAC CCA TTC AAG GAG GCT GCT CAG GAA GTA GAT AGC 2133
```

8/25

FIG. 5C.

K	L	Q	L	F	K	E	N	N	R	R	R	K	K	E	R	K	E	K	R	731
AAA	CTG	CAA	CTT	TTC	AAG	GAG	AAC	AAC	CGT	AGG	AGG	AAG	AAG	GAG	AGG	AAG	GAG	AAG	AGA	2193
R	Q	R	K	G	E	E	C	S	L	P	G	L	T	C	F	T	H	D	N	751
CGG	CAG	AGG	AAG	GGG	GAA	GAG	TGC	AGC	CTG	CCT	GGC	CTC	ACT	TGC	TTC	ACG	CAT	GAC	AAC	2253
N	H	W	Q	T	A	P	F	W	N	L	G	S	F	C	A	C	T	S	S	771
AAC	CAC	TGG	CAG	ACA	GCC	CCG	TTC	TGG	AAC	CTG	GGA	TCT	TTC	TGT	GCT	TGC	ACG	AGT	TCT	2313
N	N	N	T	Y	W	C	L	R	T	V	N	E	T	H	N	F	L	F	C	791
AAC	AAT	AAC	ACC	TAC	TGG	TGT	TTG	CGT	ACA	GTT	AAT	GAG	ACG	CAT	AAT	TTT	CTT	TTC	TGT	2373
E	F	A	T	G	F	L	E	Y	F	D	M	N	T	D	P	Y	Q	L	T	811
GAG	TTT	GCT	ACT	GGC	TTT	TTG	GAG	TAT	TTT	GAT	ATG	AAT	ACA	GAT	CCT	TAT	CAG	CTC	ACA	2433
N	T	V	H	T	V	E	R	G	I	L	N	Q	L	H	V	Q	L	M	E	831
AAT	ACA	GTG	CAC	ACG	GTA	GAA	CGA	GGC	ATT	TTG	AAT	CAG	CTA	CAC	GTA	CAA	CTA	ATG	GAG	2493
L	R	S	C	Q	G	Y	K	Q	C	N	P	R	P	K	N	L	D	V	G	851
CTC	AGA	AGC	TGT	CAA	GGA	TAT	AAG	CAG	TGC	AAC	CCA	AGA	CCT	AAG	AAT	CTT	GAT	GTT	GGA	2553
N	K	D	G	G	S	Y	D	L	H	R	G	Q	L	W	D	G	W	E	G	871
AAT	AAA	GAT	GGA	GGA	AGC	TAT	GAC	CTA	CAC	AGA	GGA	CAG	TTA	TGG	GAT	GGA	TGG	GAA	GGT	2613
*																				872
TAA																				2616

TCAGCCCCGTCTCACTGCAGACATCAACTGGCAAGGCCTAGAGGAGCTACACAGTGTGAATGAAAACATCTATGAGTAC
AGACAAAACCTACAGACTTAGTCTGGTGGACTGGACTAATTACTTGAAGGATTTAGATAGAGTATTTGCACTGCTGAAGA
GTCATATGAGCAAAATAAAACAAATAAGACTCAAAGTGCTCAAAGTGACGGGTTCTTGGTTGTCTCTGCTGAGCACGC
TGTGTCAATGGAGATGGCCTCTGCTGACTCAGATGAAGACCAAGGCATAAGGTTGGGAAAACACCTCATTGACCTTG
CCAGCTGACCTTCAAACCCTGCATTTGAACCGACCAACATTAAGTCCAGAGAGTAACTTGAATGGAATAACGACATTC
CAGAAGTTAATCATTGTAATTCTGAACACTGGAGAAAACCGAAAAATGGACGGGCATGAAGAGACTAATCATCTGGA
AACCGATTTCACTGGCGATGGCATGACAGAGCTAGAGCTCGGGCCAGCCCCAGGCTGCAGCCCATTCGAGGCACCCG
AAAGAACTTCCCCAGTATGGTGGTCTGGAAAGGACATTTTGAAGATCAACTATATCTTCTGTGCATTCCGATGGAA
TTTCAGTTTCATCAGATGTTACCATGGCCACCGCAGAACACCGAAGTAATTCAGCATAGCGGGGAAGATGTTGACCAA
GGTGGAGAAGAATCACGAAAAGGAGAAGTCACAGCACCTAGAAGGCAGCGCCTCTTCACTCTCTCTGATTAGATG
AAACTGTTACCCCTACCTAAACACAGTATTTCTTTTAACTTTTTTATTTGTAACTAATAAAGGKAATCACAGCCACC
AACATTCCAAGCTACCTGGGTACCTTTGTGCAGTAGAAGCTAGTGAGCATGTGAGCAAGCGGTGTGCACACGGAGACT
CATCGTTATAATTTACTATCTGCCAAGGAGTAGAAAGAAAGGCTGGGGATATTTGGGTTGGCTTTGGKTTTGATTTTTT
GCTTGGTTGGTTGGTTTGKACTAAACAGTATTATCTTTGAATATCGTAGGGACATAARKWWWWMMWKTTWTCMAW
YMRKAKGSYRRRAWKGGGSTYTYTSKKRKSTMWAMWYKWSMCCYSKKRWAWTYWYWMYWCYKYTSSSTGRYKRN
KTAATGAAGTT

Analysis of 23553 (871 aa)

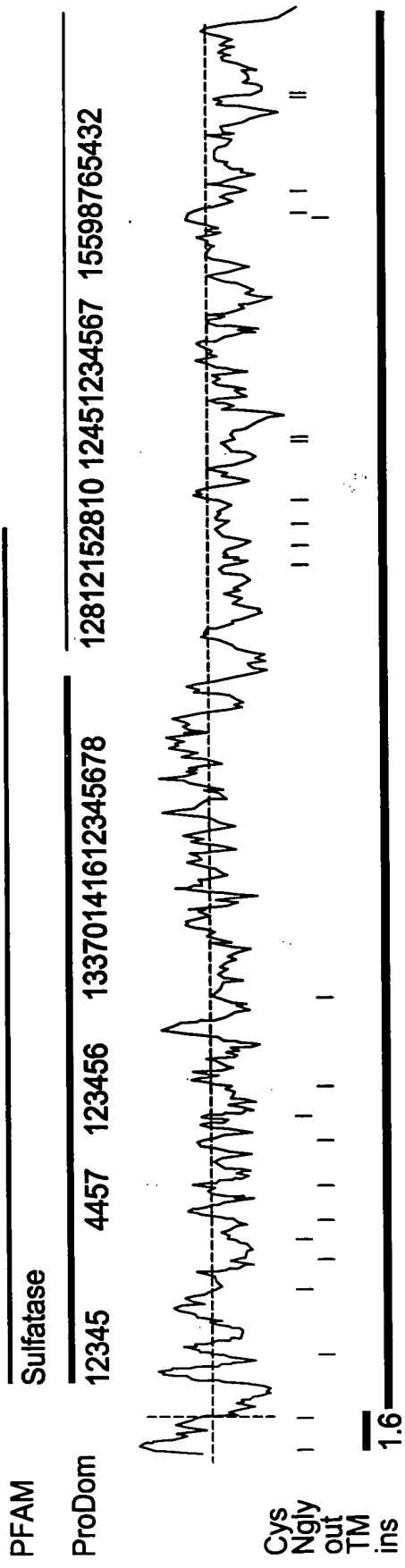


FIG. 6.

Title: 22438, 23553, 25278, and 26212,
Novel Human Sulfatases
Inventor(s): Glucksmann et al.
Application No: 09/495,823
Atty Dkt No: 5800-79(35800/191890)

10/25

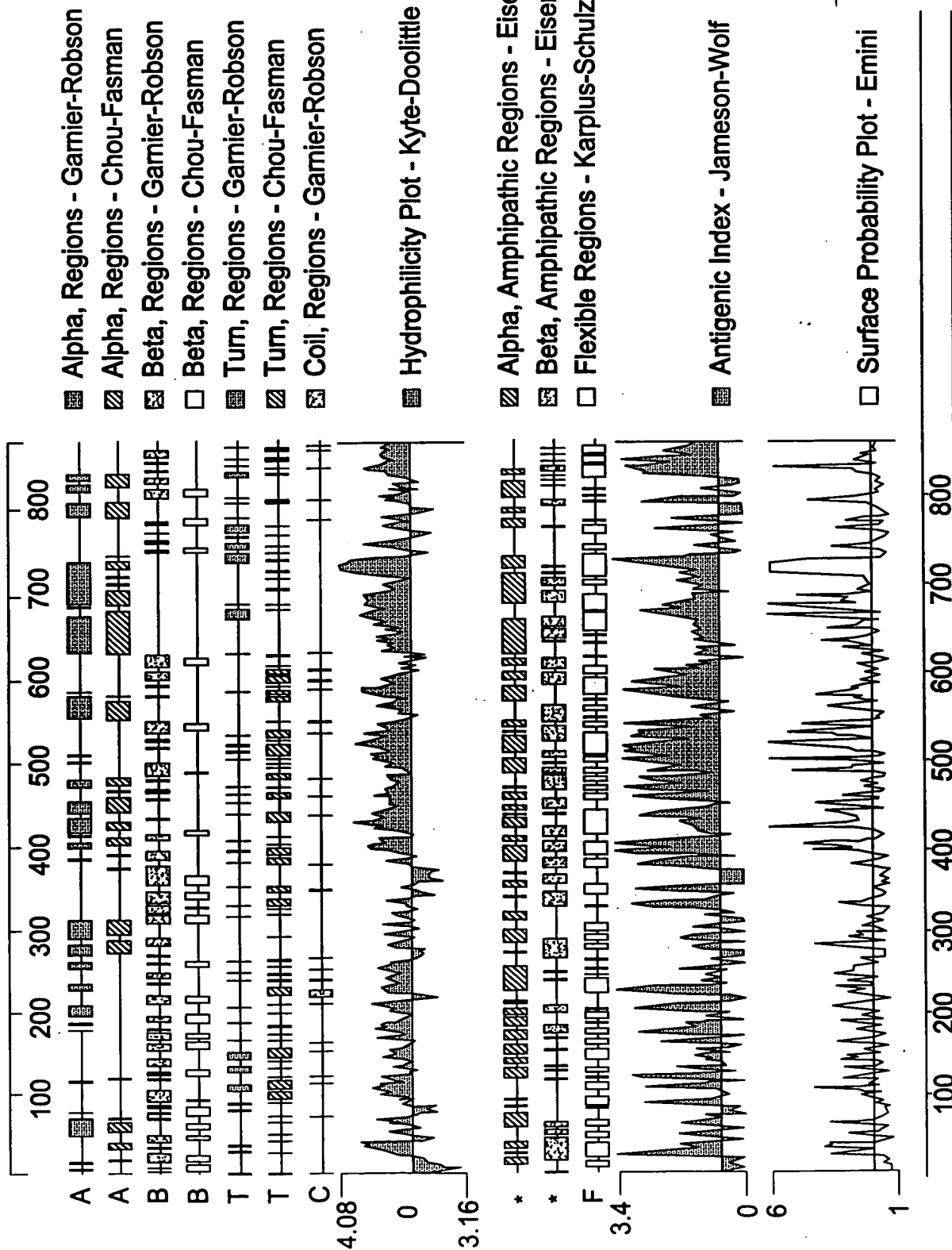


FIG. 7.

11/25

Prosite Pattern Matches for 23553

Prosite versions: Release 12.2 of February 1995

>PS00001/PDOC00001/ASN_GLYCOSYLATION N-glycosylation site.

Query: 64	NKTR	67
Query: 111	NCSS	114
Query: 131	NNTG	134
Query: 148	NGSY	151
Query: 170	NYTV	173
Query: 197	NESI	200
Query: 240	NASQ	243
Query: 623	NDSI	626
Query: 773	NNTY	776
Query: 783	NETH	786

>PS00005/PDOC00005/PKC_PHOSPHO_SITE Protein kinase C phosphorylation site.

Query: 24	TVR	26
Query: 27	SPR	29
Query: 66	TRK	68
Query: 96	TGK	98
Query: 206	SKR	208
Query: 400	TNK	402
Query: 425	SSK	427
Query: 468	SGK	470
Query: 484	TVR	486
Query: 488	STR	490
Query: 505	SCR	507
Query: 516	SQR	518
Query: 520	SQR	522
Query: 530	TPK	532
Query: 611	TVR	613
Query: 615	THK	617
Query: 635	SAR	637

>PS00006/PDOC00006/CK2_PHOSPHO_SITE Casein kinase II phosphorylation site.

Query: 107	TNNE	110
Query: 288	SVDO	291
Query: 367	TILD	370
Query: 376	TPPD	379
Query: 452	TACE	455
Query: 505	SCRE	508
Query: 781	TVNE	784

FIG. 8A.

12/25

>PS00007/PDOC00007/TYR_PHOSPHO_SITE Tyrosine kinase phosphorylation site.

Query: 637 RAWKDHKAY 645

>PS00008/PDOC00008/MYRISTYL N-myristoylation site.

Query: 19 GSLCST 24

Query: 161 GLIKNS 166

Query: 325 GLVKGK 330

Query: 592 GGNRGR 597

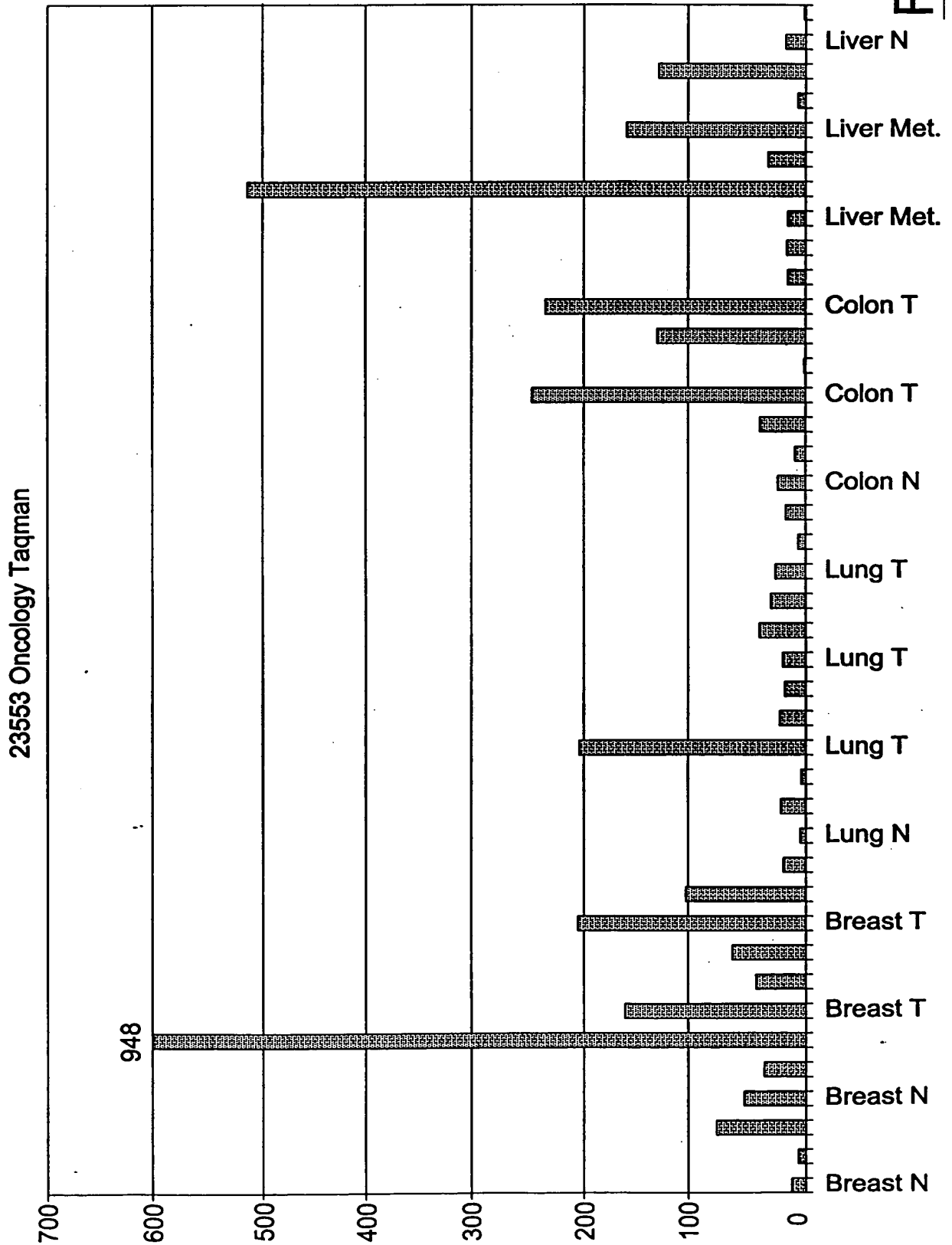
Query: 763 GSFCAC 768

Query: 851 GNKDGG 856

>PS00523/PDOC00117/SULFATASE_1 Sulfatases signature 1.

Query: 85 PMCCPSRSSMLTG 97

FIG. 8B.



14/25

FIG. 10A.

Input file Fbh25278FL1.seq; Output File: 25278.trans
Sequence length 2940

```
CCACGCGTCCGCCCACGCGTCCGGCTGCCACGCCGCTCTCAGGCTGGCCGGGCTGAGCCGGGAAGAGGGAGCAAAGG
CGGCGCAGGGCCTGCGCTTAGGCAGCGGGAGGCAGCTCGGCGCGGGCCTGACCTCCCCAGAGCGCCCCGCTGCGGCCGA
GCAGATCCGGCCCCAGCCGTCCGGCAGCCAGTCCCGGACCAGACACTGGACCGTCCCCGGGGGGCGCTGAACCTCTCGC
AGCATCCGAGCCGGCGGGCCGGTGGTGCGCCCTGGGCGCGGAGGTGGTGAGGCCCCAGGAGCCCGGCGCGCCGGGACA

      M H T L T G F S L V S L L S F      15
CGCGGGCCGGCTTGGCG ATG CAC ACC CTC ACT GGC TTC TCT CTG GTC AGC CTG CTC AGC TTC      45

G Y L S W D W A K P S F V A D G P G E A      35
GGC TAC CTG TCC TGG GAC TGG GCC AAG CCG AGC TTC GTG GCC GAC GGG CCC GGG GAG GCT      105

G E Q P S A A P P Q P P H I I F I L T D      55
GGC GAG CAG CCC TCG GCC GCT CCG CCC CAG CCT CCC CAC ATC ATC TTC ATC CTC ACG GAC      165

D Q G Y H D V G Y H G S D I E T P T L D      75
GAC CAA GGC TAC CAC GAC GTG GGC TAC CAT GGT TCA GAT ATC GAG ACC CCT ACG CTG GAC      225

R L A A K G V K L E N Y Y I Q P I C T P      95
AGG CTG GCG GCC AAG GGG GTC AAG TTG GAG AAT TAT TAC ATC CAG CCC ATC TGC ACG CCT      285

S R S Q L L T G R Y Q I H T G L Q H S I      115
TCG CGG AGC CAG CTC CTC ACT GGC AGG TAC CAG ATC CAC ACA GGA CTC CAG CAT TCC ATC      345

I R P Q Q P N C L P L D Q V T L P Q K L      135
ATC CGC CCA CAG CAG CCC AAC TGC CTG CCC CTG GAC CAG GTG ACA CTG CCA CAG AAG CTG      405

Q E A G Y S T H M V G K W H L G F Y R K      155
CAG GAG GCA GGT TAT TCC ACC CAT ATG GTG GGC AAG TGG CAC CTG GGC TTC TAC CGG AAG      465

E C L P T R R G F D T F L G S L T G N V      175
GAG TGT CTG CCC ACC CGT CGG GGC TTC GAC ACC TTC CTG GGC TCG CTC ACG GGC AAT GTG      525

D Y Y T Y D N C D G P G V C G F D L H E      195
GAC TAT TAC ACC TAT GAC AAC TGT GAT GGC CCA GGC GTG TGC GGC TTC GAC CTG CAC GAG      585

G E N V A W G L S G Q Y S T M L Y A Q R      215
GGT GAG AAT GTG GCC TGG GGG CTC AGC GGC CAG TAC TCC ACT ATG CTT TAC GCC CAG CGC      645

A S H I L A S H S P Q R P L F L Y V A F      235
GCC AGC CAT ATC CTG GCC AGC CAC AGC CCT CAG CGT CCC CTC TTC CTC TAT GTG GCC TTC      705

Q A V H T P L Q S P R E Y L Y R Y R T M      255
CAG GCA GTA CAC ACA CCC CTG CAG TCC CCT CGT GAG TAC CTG TAC CGC TAC CGC ACC ATG      765

G N V A R R K Y A A M V T C M D E A V R      275
GGC AAT GTG GCC CGG CGG AAG TAC GCG GCC ATG GTG ACC TGC ATG GAT GAG GCT GTG CGC      825

N I T W A L K R Y G F Y N N S V I I F S      295
AAC ATC ACC TGG GCC CTC AAG CGC TAC GGT TTC TAC AAC AAC AGT GTC ATC ATC TTC TCC      885

S D N G G Q T F S G G S N W P L R G R K      315
AGT GAC AAT GGT GGC CAG ACT TTC TCG GGG GGC AGC AAC TGG CCG CTC CGA GGA CGC AAG      945

G T Y W E G G V R G L G F V H S P L L K      335
GGC ACT TAT TGG GAA GGT GGC GTG CGG GGC CTA GGC TTT GTC CAC AGT CCC CTG CTC AAG      1005
```

15/25

R	K	Q	R	T	S	R	A	L	M	H	I	T	D	W	Y	P	T	L	V	355
CCA	AAG	CAA	CGG	ACA	AGC	CGG	GCA	CTG	ATG	CAC	ATC	ACT	GAC	TGG	TAC	CCG	ACC	CTG	GTG	1065
G	L	A	G	G	T	T	S	A	A	D	G	L	D	G	Y	D	V	W	P	375
GGT	CTG	GCA	GGT	GGT	ACC	ACC	TCA	GCA	GCC	GAT	GGG	CTA	GAT	GGC	TAC	GAC	GTG	TGG	CCG	1125
A	I	S	E	G	R	A	S	P	R	T	E	I	L	H	N	I	D	P	L	395
GCC	ATC	AGC	GAG	GGC	CGG	GCC	TCA	CCA	CGC	ACG	GAG	ATC	CTG	CAC	AAC	ATT	GAC	CCA	CTC	1185
Y	N	H	A	Q	H	G	S	L	E	G	G	F	G	I	W	N	T	A	V	415
TAC	AAC	CAT	GCC	CAG	CAT	GGC	TCC	CTG	GAG	GGC	GGC	TTT	GGC	ATC	TGG	AAC	ACC	GCC	GTG	1245
Q	A	A	I	R	V	G	E	W	K	L	L	T	G	D	P	G	Y	G	D	435
CAG	GCT	GCC	ATC	CGC	GTG	GGT	GAG	TGG	AAG	CTG	CTG	ACA	GGA	GAC	CCC	GGC	TAT	GGC	GAT	1305
W	I	P	P	Q	T	L	A	T	F	P	G	S	W	W	N	L	E	R	M	455
TGG	ATC	CCA	CCG	CAG	ACA	CTG	GCC	ACC	TTC	CCG	GGT	AGC	TGG	TGG	AAC	CTG	GAA	CGA	ATG	1365
A	S	V	R	Q	A	V	W	L	F	N	I	S	A	D	P	Y	E	R	E	475
GCC	AGT	GTC	CGC	CAG	GCC	GTG	TGG	CTC	TTC	AAC	ATC	AGT	GCT	GAC	CCT	TAT	GAA	CGG	GAG	1425
D	L	A	G	Q	R	P	D	V	V	R	T	L	L	A	R	L	A	E	Y	495
GAC	CTG	GCT	GGC	CAG	CGG	CCT	GAT	GTG	GTC	CGC	ACC	CTG	CTG	GCT	CGC	CTG	GCC	GAA	TAT	1485
N	R	T	A	I	P	V	R	Y	P	A	E	N	P	R	A	H	P	D	F	515
AAC	CGC	ACA	GCC	ATC	CCG	GTA	CGC	TAC	CCA	GCT	GAG	AAC	CCC	CGG	GCT	CAT	CCT	GAC	TTT	1545
N	G	G	A	W	G	P	W	A	S	D	E	E	E	E	E	E	E	G	R	535
AAT	GGG	GGT	GCT	TGG	GGG	CCC	TGG	GCC	AGT	GAT	GAG	GAA	GAG	GAG	GAA	GAG	GAA	GGG	AGG	1605
A	R	S	F	S	R	G	R	R	K	K	K	C	K	I	C	K	L	R	S	555
GCT	CGA	AGC	TTC	TCC	CGG	GGT	CGT	CGC	AAG	AAA	AAA	TGC	AAG	ATT	TGC	AAG	CTT	CGA	TCC	1665
F	F	R	K	L	N	T	R	L	M	S	Q	R	I	*						570
TTT	TTC	CGT	AAA	CTC	AAC	ACC	AGG	CTA	ATG	TCC	CAA	CGG	ATC	TGA						1710

TGGTGGGGAGGGAGAAAAGTGTCTTTAGAGGATCTTCCCACTCCGGCTTGGCCCTGCTGTTTCTCAGGGAGAAGCCT
 GTCACATCTCCATCTACAGGGAGTTGGAGGGGTAGAGTCCCTTGGTTGAACAGGGTAGGGAGCCTGGATAGGAGTGGG
 TGGGAATAAACCAGACTGGGATGCCTGTGTCTCAGTCTGCTCCTCCTCAGGACTTGCTCTGTGACCTCAGGTGACCCAC
 ATGAGCTTTTAGCCTCAGTTTCCTCATCTGTAAATGAGCTCTAATGACTTTGTGACTCTTTGGTGTGGCCCTGGAGCC
 TGGGGCCACGGTGGAGTTCTTGGCCGGCCTTGCCACTTGACAACCTTTAAGGCTTCCCCCTTAACACGGGATCCCTG
 TGGTGGTGTGGGAGTTGCCTGGAGGCAACTCCAAGCCTGGCCCCAGCTGAAGCATGGCAATCTGGCTGCTCTCTAC
 AGGGACCCCCAAGCGCTGTGGGTGGAGGGCAGGGGTGGGGGGGTGACCTTCTTGGGTCTTCACATGGCCTAGGCCAG
 TCCTCCGGTCAGACTGGTGTGAGGCACCGTGGTGCAAAATTCCTCTTCTGGCCCCCAGTACCCAGAGAACTGGCTG
 GGCCATTAAGTGTGAGCACCAAGGGTGGTAGAAGAGCTGTGAAGAGCCCCCAACAGTACCAGGACACCTGGGTT
 CTCCTGTGACCTGGGGCACAGTTCTTGGCCCTTAGGCCTTGATTTCCCCACCTGCAAGTGGGGATGCCAGCCCTGGCTC
 TGCCCTTCATGAGGCTCTGGAAGACTGGCCAAGGTTGTGGAGGAGCTTGTAAGTGGATTAAAGTGTGTAACATGG
 AAAAAAAAAAAAAAAAAAAAAAGGGCGG

FIG. 10B.

Analysis of 25278 (569 aa)

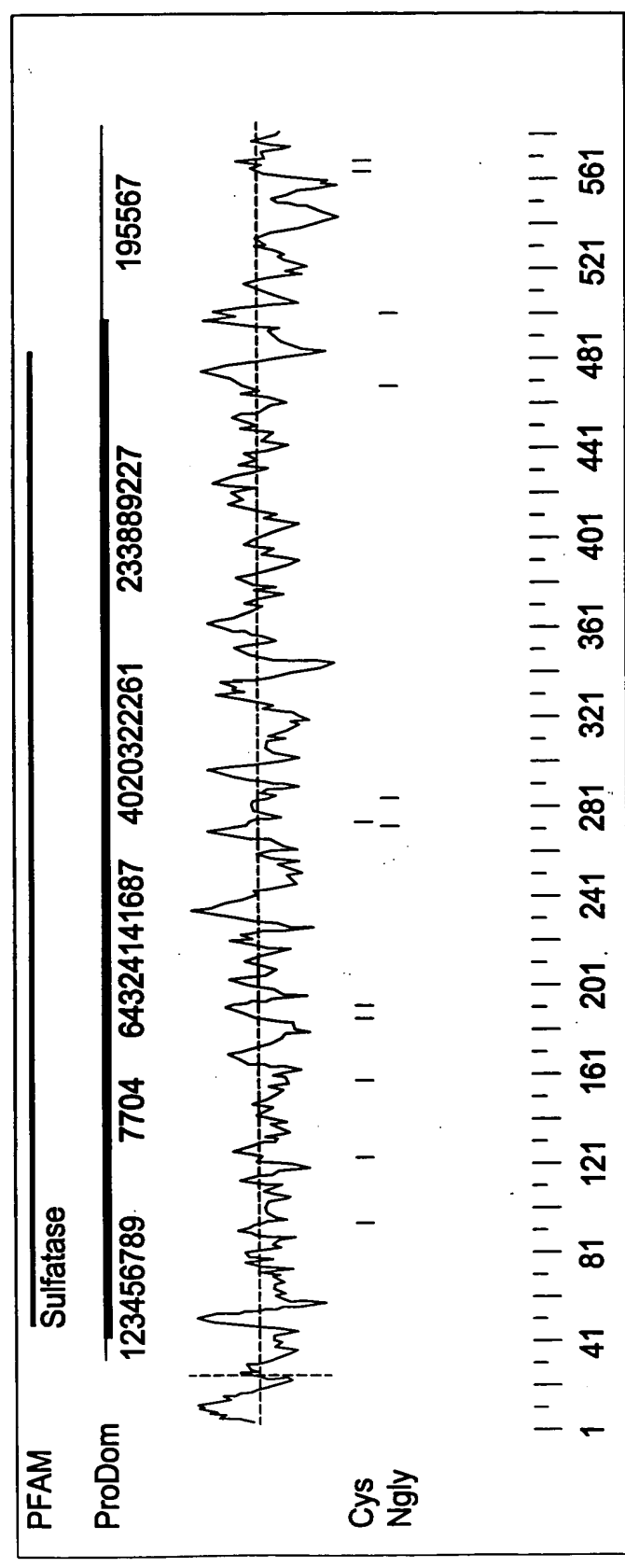
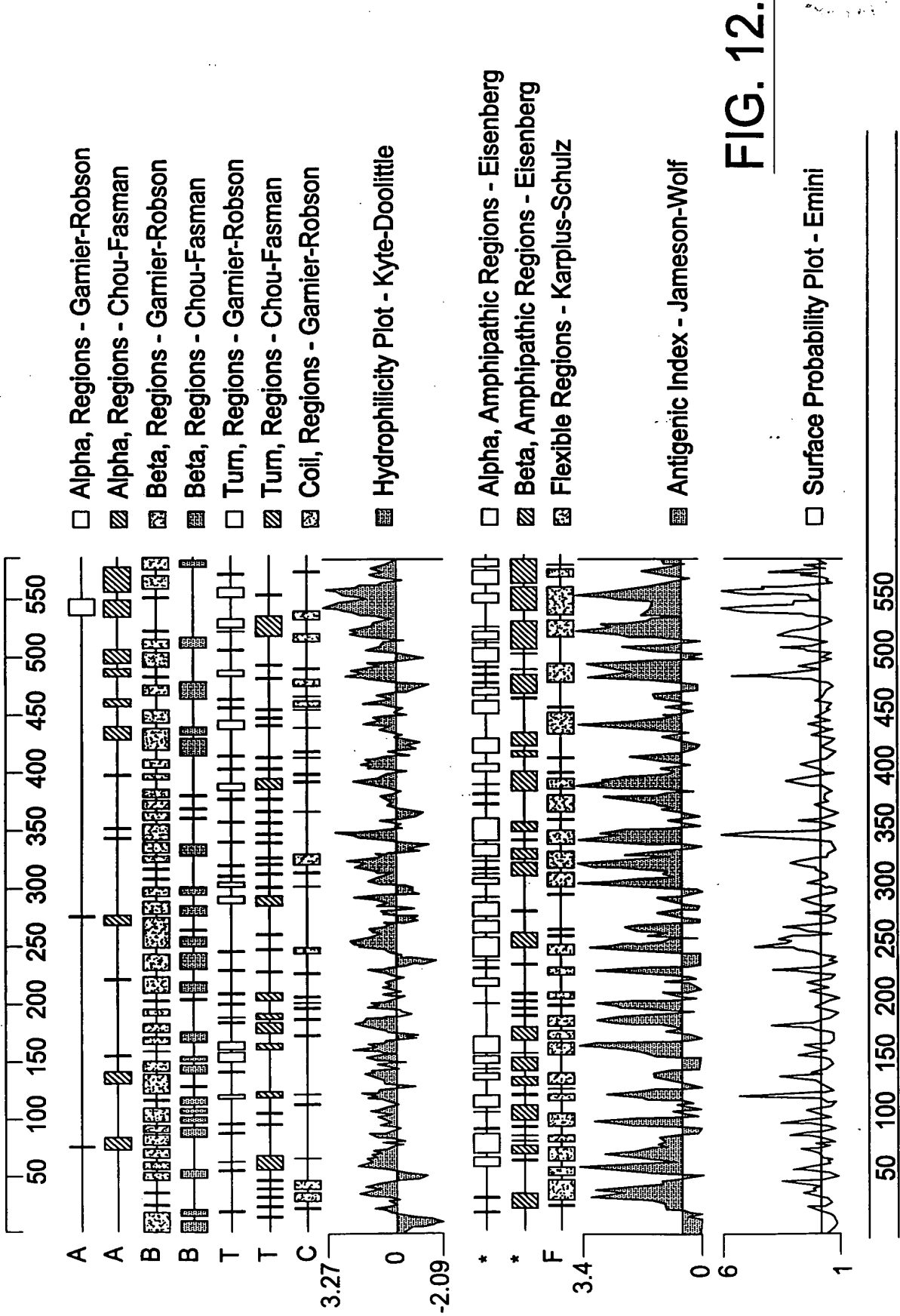


FIG. 11.



18/25

FIG. 13.

Prosite Pattern Matches for 25278

Prosite versions: Release 12.2 of February 1995

>PS00001/PDOC00001/ASN_GLYCOSYLATION N-glycosylation site.

Query: 276 NITW 279

Query: 288 NNSV 291

Query: 466 NISA 469

Query: 496 NRTA 499

>PS00004/PDOC00004/CAMP_PHOSPHO_SITE cAMP- and cGMP-dependent protein kinase phosphorylation site.

Query: 314 RKGT 317

>PS00005/PDOC00005/PKC_PHOSPHO_SITE Protein kinase C phosphorylation site.

Query: 102 TGR 104

Query: 160 TRR 162

Query: 244 SPR 246

Query: 340 TSR 342

Query: 383 SPR 385

Query: 457 SVR 459

Query: 566 SQR 568

>PS00006/PDOC00006/CK2_PHOSPHO_SITE Casein kinase II phosphorylation site.

Query: 67 SDIE 70

Query: 244 SPRE 247

Query: 268 TCMD 271

Query: 317 TYWE 320

Query: 363 SAAD 366

Query: 525 SDEE 528

>PS00007/PDOC00007/TYR_PHOSPHO_SITE Tyrosine kinase phosphorylation site.

Query: 134 KLQEAGY 140

>PS00008/PDOC00008/MYRISTYL N-myristoylation site.

Query: 110 GLQHSI 115

Query: 169 GSLTGN 174

Query: 205 GQYSTM 210

Query: 300 GQTFSG 305

Query: 321 GGVRL 326

Query: 356 GLAGGT 361

Query: 402 GSLEGG 407

Query: 409 GIWNTA 414

Query: 447 GSWWNL 452

>PS00009/PDOC00009/AMIDATION Amidation site.

Query: 312 RGRK 315

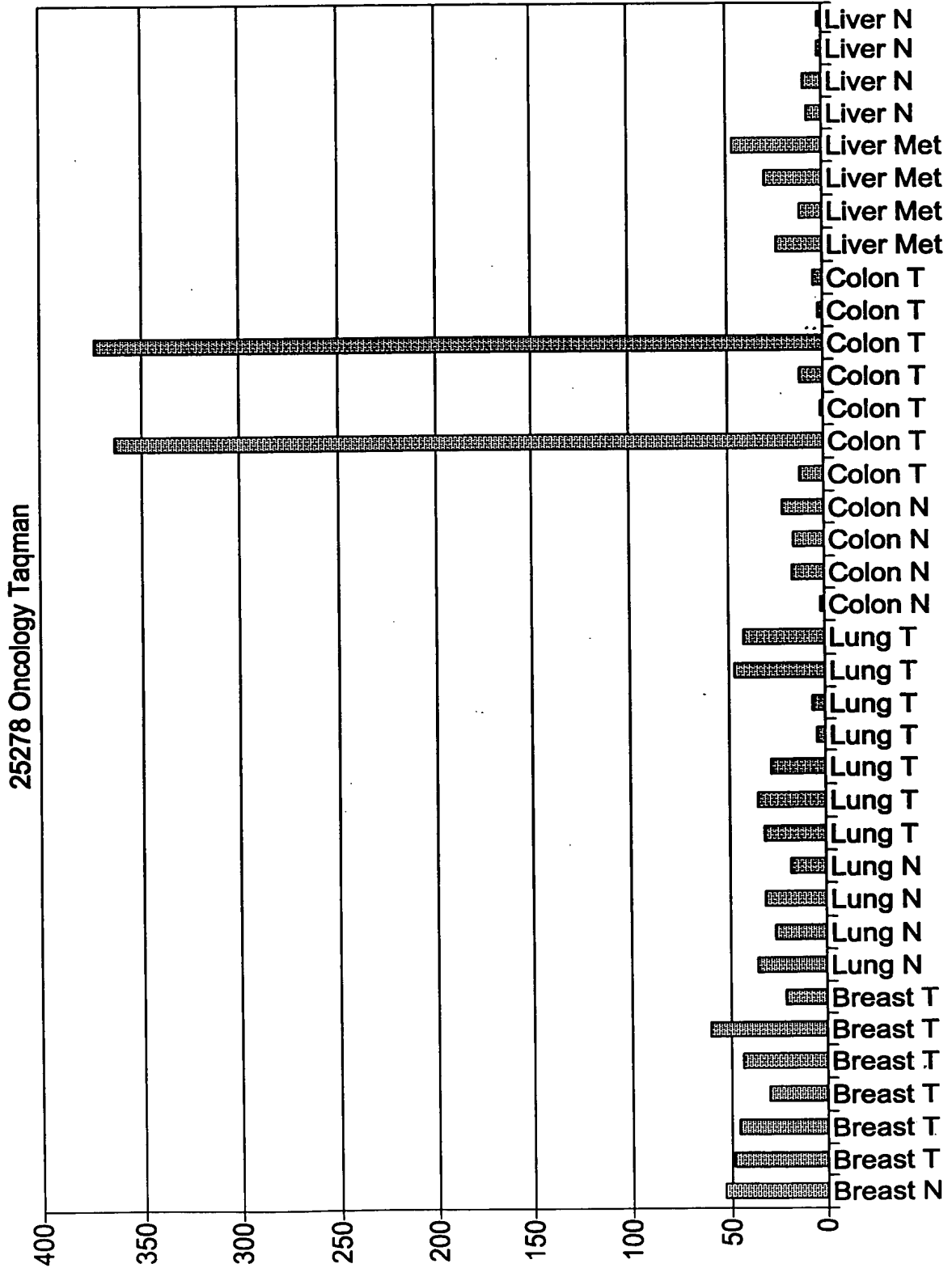
Query: 541 RGRR 544

>PS00149/PDOC00117/SULFATASE_2 Sulfatases signature 2.

Query: 139 GYSTHMGKW 148

>PS00523/PDOC00117/SULFATASE_1 Sulfatases signature 1.

Query: 91 PICTPSRSQLLTG 103



20/25

Input file 26212cons; Output File 26212pat
Sequence length 2266

```
CACGCGTCCGCCACGCGTCCGTGGAGATATTAACTTTTTCTTTTTTTTTTTCCTTGGTGAAGCTGCTCTAGGGAGG
GGGGAGGAGGAGGAGAAAGTGAAATGTGCTGGAGAAGAGCGAGCCCTCCTTGTCTTCCGGAGTCCCATCCATTAAGCC
ATCACTTCTGGAAGATTAAAGTTGTCTGGACATGGTGACAGCTGAGAGGAGAGGAGGATTCTTGCCAGGTGGAGAGTCT
TCACCGTCTGTTGGGTGCATGTGTGCCCGCCGASCAGCGCGGGGCGCGTGGTTCTCCGCGTGGAGTCTCACCTGGGACC

      M  A  P  R  G  C  A  G  H  P  P  P  P  S  P  Q  A  C      18
TGAGTGA ATG GCT CCC AGG GGC TGT GCG GGG CAT CCG CCT CCG CCT TCT CCA CAG GCC TGT      54

V  C  P  G  K  M  L  A  M  G  A  L  A  G  F  W  I  L  C  L      38
GTC TGT CCT GGA AAG ATG CTA GCA ATG GGG GCG CTG GCA GGA TTC TGG ATC CTC TGC CTC      114

L  T  Y  G  Y  L  S  W  G  Q  A  L  E  E  E  E  E  E  G  A  L      58
CTC ACT TAT GGT TAC CTG TCC TGG GGC CAG GCC TTA GAA GAG GAG GAA GAA GGG GCC TTA      174

L  A  Q  A  G  E  K  L  E  P  S  T  T  S  T  S  Q  P  H  L      78
CTA GCT CAA GCT GGA GAG AAA CTA GAG CCC AGC ACA ACT TCC ACC TCC CAG CCC CAT CTC      234

I  F  I  L  A  D  D  Q  G  F  R  D  V  G  Y  H  G  S  E  I      98
ATT TTC ATC CTA GCG GAT GAT CAG GGA TTT AGA GAT GTG GGT TAC CAC GGA TCT GAG ATT      294

K  T  P  T  L  D  K  L  A  A  E  G  V  K  L  E  N  Y  Y  V      118
AAA ACA CCT ACT CTT GAC AAG CTC GCT GCC GAA GGA GTT AAA CTG GAG AAC TAC TAT GTC      354

Q  P  I  C  T  P  S  R  S  Q  F  I  T  G  K  Y  Q  I  H  T      138
CAG CCT ATT TGC ACA CCA TCC AGG AGT CAG TTT ATT ACT GGA AAG TAT CAG ATA CAC ACC      414

G  L  Q  H  S  I  I  R  P  T  Q  P  N  C  L  P  L  D  N  A      158
GGA CTT CAA CAT TCT ATC ATA AGA CCT ACC CAA CCC AAC TGT TTA CCT CTG GAC AAT GCC      474

T  L  P  Q  K  L  K  E  V  G  Y  S  T  H  M  V  G  K  W  H      178
ACC CTA CCT CAG AAA CTG AAG GAG GTT GGA TAT TCA ACG CAT ATG GTC GGA AAA TGG CAC      534

L  G  F  Y  R  K  E  C  M  P  T  R  R  G  F  D  T  F  F  G      198
TTG GGT TTT TAC AGA AAA GAA TGC ATG CCC ACC AGA AGA GGA TTT GAT ACC TTT TTT GGT      594

S  L  L  G  S  G  D  Y  Y  T  H  Y  K  C  D  S  P  G  M  C      218
TCC CTT TTG GGA AGT GGG GAT TAC TAT ACA CAC TAC AAA TGT GAC AGT CCT GGG ATG TGT      654

G  Y  D  L  Y  E  N  D  N  A  A  W  D  Y  D  N  G  I  Y  S      238
GGC TAT GAC TTG TAT GAA AAC GAC AAT GCT GCC TGG GAC TAT GAC AAT GGC ATA TAC TCC      714

T  Q  M  Y  T  Q  R  V  Q  Q  I  L  A  S  H  N  P  T  K  P      258
ACA CAG ATG TAC ACT CAG AGA GTA CAG CAA ATC TTA GCT TCC CAT AAC CCC ACA AAG CCT      774

I  F  L  Y  I  A  Y  Q  A  V  H  S  P  L  Q  A  P  G  R  Y      278
ATA TTT TTA TAT ATT GCC TAT CAA GCT GTT CAT TCA CCA CTG CAA GCT CCT GGC AGG TAT      834

F  E  H  Y  R  S  I  I  N  I  N  R  R  R  Y  A  A  M  L  S      298
TTC GAA CAC TAC CGA TCC ATT ATC AAC ATA AAC AGG AGG AGA TAT GCT GCC ATG CTT TCC      894

C  L  D  E  A  I  N  N  V  T  L  A  L  K  T  Y  G  F  Y  N      318
TGC TTA GAT GAA GCA ATC AAC AAC GTG ACA TTG GCT CTA AAG ACT TAT GGT TTC TAT AAC      954
```

FIG. 15A.

21/25

N	S	I	I	I	Y	S	S	<u>D</u>	<u>N</u>	<u>G</u>	<u>G</u>	<u>Q</u>	P	T	A	G	G	S	<u>N</u>	338
AAC	AGC	ATT	ATC	ATT	TAC	TCT	TCA	GAT	AAT	GGT	GGC	CAG	CCT	ACG	GCA	GGA	GGG	AGT	AAC	1014
W	P	L	R	G	S	K	G	T	Y	<u>W</u>	<u>E</u>	<u>G</u>	<u>G</u>	<u>I</u>	<u>R</u>	A	V	G	F	358
TGG	CCT	CTC	AGA	GGT	AGC	AAA	GGA	ACA	TAT	TGG	GAA	GGA	GGG	ATC	CGG	GCT	GTA	GGC	TTT	1074
V	H	<u>S</u>	<u>P</u>	<u>L</u>	<u>L</u>	<u>K</u>	N	K	G	T	V	C	K	E	L	V	H	I	T	378
GTG	CAT	AGC	CCA	CTT	CTG	AAA	AAC	AAG	GGA	ACA	GTG	TGT	AAG	GAA	CTT	GTG	CAC	ATC	ACT	1134
D	W	Y	P	T	L	I	S	L	A	E	G	Q	I	D	E	D	I	Q	L	398
GAC	TGG	TAC	CCC	ACT	CTC	ATT	TCA	CTG	GCT	GAA	GGA	CAG	ATT	GAT	GAG	GAC	ATT	CAA	CTA	1194
D	G	Y	D	I	W	E	<u>T</u>	<u>I</u>	<u>S</u>	<u>E</u>	<u>G</u>	L	R	S	P	R	V	D	I	418
GAT	GGC	TAT	GAT	ATC	TGG	GAG	ACC	ATA	AGT	GAG	GGT	CTT	CGC	TCA	CCC	CGA	GTA	GAT	ATT	1254
L	H	N	I	D	<u>P</u>	I	Y	T	K	A	K	N	G	S	W	A	A	G	Y	438
TGG	CAT	AAC	ATT	GAC	CCC	ATA	TAC	ACC	AAG	GCA	AAA	AAT	GGC	TCC	TGG	GCA	GCA	GGC	TAT	1314
G	I	W	N	T	A	I	Q	S	A	I	R	V	Q	H	<u>W</u>	<u>K</u>	<u>L</u>	<u>L</u>	<u>T</u>	458
GGG	ATC	TGG	AAC	ACT	GCA	ATC	CAG	TCA	GCC	ATC	AGA	GTG	CAG	CAC	TGG	AAA	TTG	CTT	ACA	1374
<u>G</u>	N	P	G	Y	S	D	W	V	P	P	Q	S	F	S	N	L	G	P	N	478
GGA	AAT	CCT	GGC	TAC	AGC	GAC	TGG	GTC	CCC	CCT	CAG	TCT	TTC	AGC	AAC	CTG	GGA	CCG	AAC	1434
R	W	H	N	E	R	I	T	S	S	T	G	K	S	V	W	L	F	N	I	498
CGG	TGG	CAC	AAT	GAA	CGG	ATC	ACC	TCG	TCA	ACT	GGC	AAA	AGT	GTA	TGG	CTT	TTC	AAC	ATC	1494
T	A	D	P	Y	E	R	V	D	L	S	N	R	Y	P	G	I	V	K	K	518
ACA	GCC	GAC	CCA	TAT	GAG	AGG	GTG	GAC	CTA	TCT	AAC	AGG	TAT	CCA	GGA	ATC	GTG	AAG	AAG	1554
L	L	R	R	L	S	Q	F	N	K	T	A	V	P	V	R	Y	P	P	K	538
CTC	CTA	CGG	AGG	CTC	TCA	CAG	TTC	AAC	AAA	ACT	GCA	GTG	CCG	GTC	AGG	TAT	CCC	CCC	AAA	1614
D	P	R	S	N	P	R	L	N	G	G	V	*								551
GAC	CCC	AGA	AGT	AAC	CCT	AGG	CTC	AAT	GGA	GGG	GTC	TAG								1653

GGACCATGGTATAGAGAGGAAACCAAGAAAAAGAAGCCAAGCAAAAATCAGGCTGAGAAAAAGCAAAAGAAAAGCAAAA
 AAAGAAGAAGAAACAGCAGAAAGCAGTCTCAGGTTCAACTTGCCATTCAGGTGTTACTTGTGGATAAGCACAAATATTT
 CCTGTTTGGTTAAACTTTAATCAGTTCTTATCTTTTCATCTGTTTCCTAGGTAAACCAGCAAATTTGGCTCGATAATATC
 GCTGGCCTAAGCGTCAGGCTTGTTTTTCATGCTGTGCCACCTGGTGCCGAATTC

FIG. 15B.

22/25

Analysis of 26212prot (550 aa)

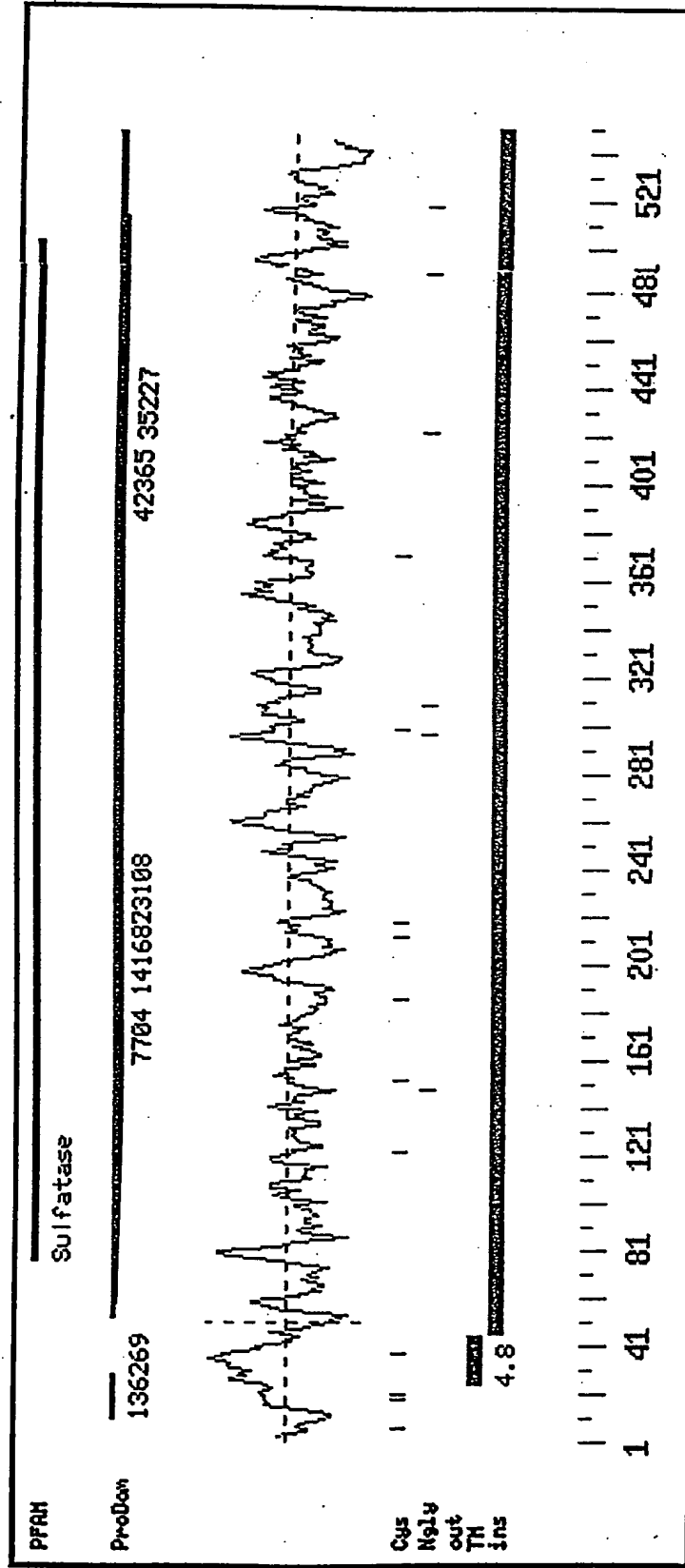
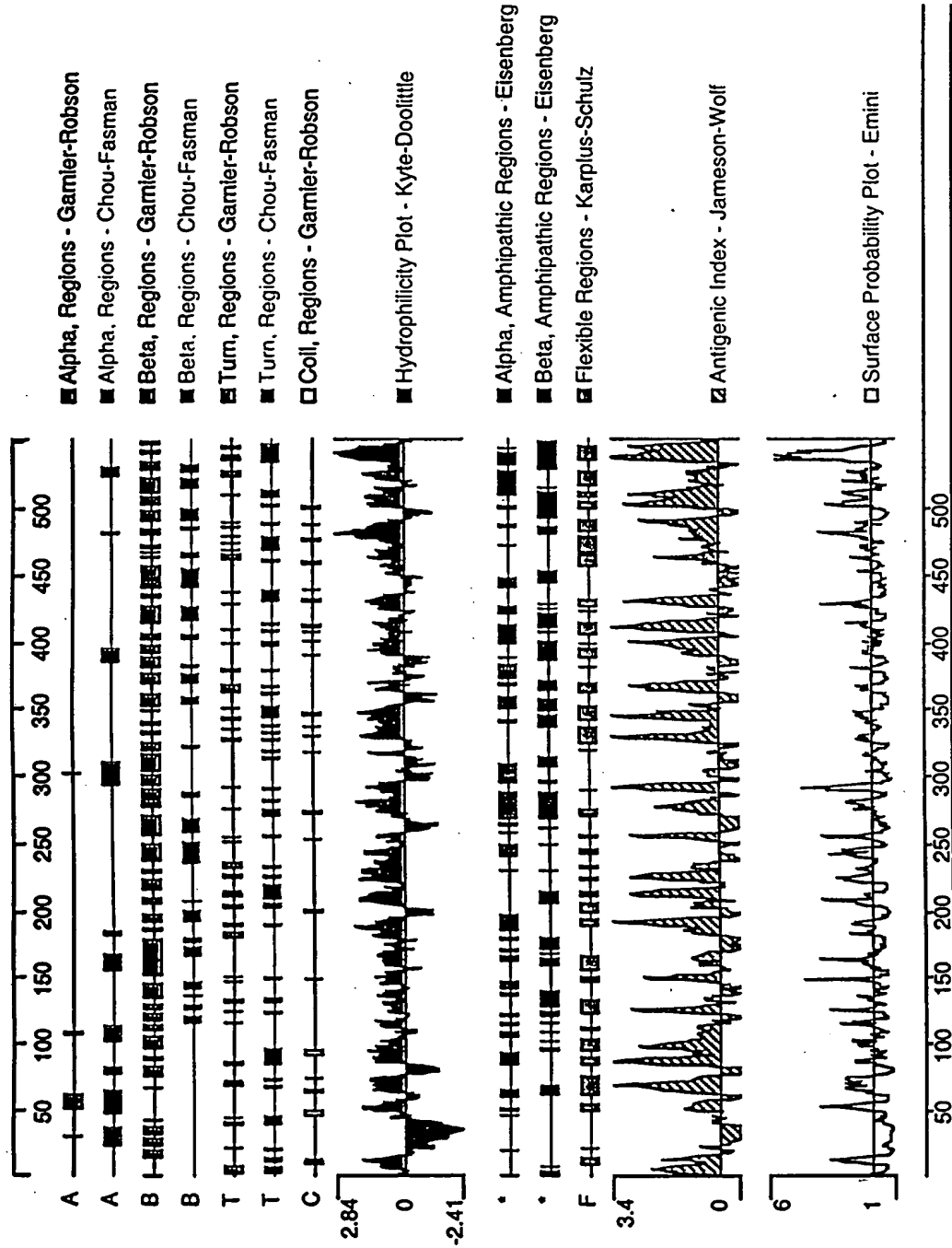


FIG. 16.

FIG. 17.



24/25

Prosite Pattern Matches for 26212prot

Prosite version: Release 12.2 of February 1995

>PS00001|PDOC00001|ASN_GLYCOSYLATION N-glycosylation site.

Query: 157 NATL 160

Query: 306 NVTL 309

Query: 318 NNSI 321

Query: 431 NGSW 434

Query: 497 NITA 500

Query: 527 NKTA 530

>PS00004|PDOC00004|CAMP_PHOSPHO_SITE cAMP- and cGMP-dependent
protein kinase phosphorylation site.

Query: 521 RRLS 524

>PS00005|PDOC00005|PKC_PHOSPHO_SITE Protein kinase C
phosphorylation site.

Query: 131 TGK 133

Query: 189 TRR 191

Query: 243 TQR 245

Query: 413 SPR 415

Query: 489 TGK 491

Query: 509 SNR 511

FIG. 18A.

25/25

>PS000006|PDOC00006|CK2_PHOSPHO_SITE Casein kinase II phosphorylation site.

Query: 298 SCLD 301

Query: 347 TYWE 350

Query: 386 SLAE 389

Query: 406 TISE 409

>PS000007|PDOC00007|TYR_PHOSPHO_SITE Tyrosine kinase phosphorylation site.

Query: 163 KLKEVGY 169

>PS000008|PDOC00008|MYRISTYL N-myristoylation site.

Query: 28 GALAGF 33

Query: 56 GALLAQ 61

Query: 139 GLQHSI 144

Query: 198 GSLLGS 203

Query: 235 GIYSTQ 240

Query: 329 GGQPTA 334

Query: 343 GSKGTY 348

Query: 351 GGIRAV 356

Query: 432 GSWAAG 437

Query: 439 GIWNTA 444

>PS00149|PDOC00117|SULFATASE_2 Sulfatases signature 2.

Query: 168 GYSTHMGKW 177

>PS00523|PDOC00117|SULFATASE_1 Sulfatases signature 1.

Query: 120 PICTPSRSQFITG 132

FIG. 18B.